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OM nucleic - nucleic search, using sw model

Run on: January 17, 2005, 12:56:43 ; Search time 2206.61 Seconds.
(without alignments)
16548.056 Million cell updates/sec

Title: US-09-551-494-5
Perfect score: 6355
Sequence: 1 gatgttttaatagttttoga.....taacgcggttagcgccca 6355

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues
Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6355	100.0	6355	US-10-321-434-7	Sequence 7, Appli
2	2468	38.8	6395	US-09-962-527-1	Sequence 1, Appli
3	2468	38.8	6395	US-10-828-029-1	Sequence 1, Appli
4	2466.4	38.8	6395	US-10-338-592-2	Sequence 2, Appli
5	2455.4	38.6	6439	US-09-962-527-2	Sequence 2, Appli
6	2455.4	38.6	6439	US-10-828-029-2	Sequence 2, Appli
7	2452.2	38.6	6475	US-09-962-527-4	Sequence 4, Appli
8	2452.2	38.6	6475	US-10-828-029-4	Sequence 4, Appli
9	2449.8	38.5	6446	US-09-962-527-5	Sequence 5, Appli
10	2449.8	38.5	6446	US-10-828-029-5	Sequence 5, Appli
11	2431.2	38.3	6425	US-09-962-527-3	Sequence 3, Appli
12	2431.2	38.3	6425	US-10-828-029-3	Sequence 3, Appli

13	2291.4	36.1	11222	17	US-10-679-620-73	Sequence 73, Appli
14	2291.4	36.1	11641	9	US-09-993-059-33	Sequence 33, Appli
15	2291.4	36.1	11641	15	US-10-103-327-33	Sequence 33, Appli
16	2291.4	36.1	11641	16	US-10-684-300-13	Sequence 13, Appli
17	2291.4	36.1	11641	16	US-10-684-349-13	Sequence 13, Appli
18	2291.4	36.1	11641	18	US-10-851-388-33	Sequence 33, Appli
19	2289.8	36.0	10600	15	US-10-356-708-1	Sequence 1, Appli
20	2289.8	36.0	10600	17	US-10-280-913A-1	Sequence 1, Appli
21	2289.8	36.0	10600	17	US-10-684-134-1	Sequence 1, Appli
22	2289.8	36.0	10600	17	US-10-637-758-1	Sequence 1, Appli
23	2289.8	36.0	10624	15	US-10-356-708-2	Sequence 2, Appli
24	2289.8	36.0	10624	17	US-10-280-913A-2	Sequence 2, Appli
25	2289.8	36.0	10624	17	US-10-684-134-2	Sequence 2, Appli
26	2289.8	36.0	10624	17	US-10-637-758-2	Sequence 2, Appli
27	2286.6	36.0	7685	9	US-09-949-317-22	Sequence 22, Appli
28	2286.6	36.0	7685	9	US-09-949-317-25	Sequence 25, Appli
29	2286.6	36.0	7685	9	US-09-949-316-22	Sequence 22, Appli
30	2286.6	36.0	7685	9	US-09-949-316-25	Sequence 25, Appli
31	2286.6	36.0	7685	14	US-10-200-051-22	Sequence 22, Appli
32	2286.6	36.0	7685	14	US-10-200-051-25	Sequence 25, Appli
33	2286.6	36.0	7686	9	US-09-949-317-23	Sequence 23, Appli
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38	2286.6	36.0	7687	14	US-10-200-051-24	Sequence 24, Appli
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41	2286.6	36.0	7688	14	US-10-200-051-27	Sequence 27, Appli
42	2286.6	36.0	10132	9	US-09-978-199-3	Sequence 3, Appli
43	2285	36.0	7926	14	US-10-119-330-1	Sequence 1, Appli
44	2285	36.0	7926	16	US-10-632-240-1	Sequence 1, Appli
45	2285	36.0	10607	15	US-10-098-155-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-321-434-7
; Sequence 7, Application US/10321434
; Publication No. US20030135882A1
; GENERAL INFORMATION:
; APPLICANT: Metzlaff, Michael
; APPLICANT: Meulewater, Frank
; APPLICANT: Gosse, Veronique
; APPLICANT: Fach, Ina
; TITLE OF INVENTION: Improved methods and means for delivering inhibitory RNA to plan
; FILE REFERENCE: PKMOD
; CURRENT APPLICATION NUMBER: US/10/321,434
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 6355
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: cdna sequence of the genome of TMV-U2
US-10-321-434-7

Query Match	100.0%	Score 6355	DB 15	Length 6355
Best Local Similarity	100.0%	Pred. No. 0		
Matches 6355	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Db	1	GATGTTTTTAATAGTTTCGACAAACAAATTTAAACAAACAAACATATTACAAACA 60		
QY	61	AACAAACAATGGGACACATCAATCTATAATTAGCAACGCCCTTCTTGAAGCGTGAG 120		
Db	61	AACAAACAATGGGACACATCAATCTATAATTAGCAACGCCCTTCTTGAAGCGTGAG 120		

QY	121	TGTTAAACACCTCTCGTTAAATGACCTTGCAGAGGCGCATGTACGATACGGCGTGGA	180
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QY	181	AGAAATTTAAAGCGCGCGAGCGGTAGACCAAGGTCAACTTTTCCAAACCTATTAGCGAAGA	240
DB	181	AGAAATTTAAAGCGCGCGAGCGGTAGACCAAGGTCAACTTTTCCAAACCTATTAGCGAAGA	240
QY	241	GCAACGCTTCTAGTCTCAACGCGTACCGGAGTTCCAGATTACCTTTTATAAFACTCA	300
DB	241	GCAACGCTTCTAGTCTCAACGCGTACCGGAGTTCCAGATTACCTTTTATAAFACTCA	300
QY	301	AAATGCCGTACACAGTTTGGCTGGAGTTTGAGAGCAATTAGAAATCTGATGCT	360
DB	301	AAATGCCGTACACAGTTTGGCTGGAGTTTGAGAGCAATTAGAAATCTGATGCT	360
QY	361	ACAAGTTCCTATGGATCCGACATATGATATAGGTGGAACTTTGACAGCACTTTGTT	420
DB	361	ACAAGTTCCTATGGATCCGACATATGATATAGGTGGAACTTTGACAGCACTTTGTT	420
QY	421	CAAAGCAGGGATTACGTGCATTGTGTATGCCAATCTGGACATACGAGATATAATGAG	480
DB	421	CAAAGCAGGGATTACGTGCATTGTGTATGCCAATCTGGACATACGAGATATAATGAG	480
QY	481	GCACGAGGACAAAGGACTCAATTGAGATGATTTGTCAGATTTGCTCGTTCTTAACAA	540
DB	481	GCACGAGGACAAAGGACTCAATTGAGATGATTTGTCAGATTTGCTCGTTCTTAACAA	540
QY	541	GGTAAATTCCTGAGTTTCAAAGGAGGCTTTTAAACAGGTATGCAAGACTCCCAACGAAGT	600
DB	541	GGTAAATTCCTGAGTTTCAAAGGAGGCTTTTAAACAGGTATGCAAGACTCCCAACGAAGT	600
QY	601	CTGCTGCTCTAAACCTTTTCAAGGATGTGCAATACATCCGCCAGAGAAATAGTGGTAGAAG	660
DB	601	CTGCTGCTCTAAACCTTTTCAAGGATGTGCAATACATCCGCCAGAGAAATAGTGGTAGAAG	660
QY	661	ATACGCTGTGCTCCGACAGTTTGTATGATATTCCTGTCGATGAGTTTGGAGCTCGGTT	720
DB	661	ATACGCTGTGCTCCGACAGTTTGTATGATATTCCTGTCGATGAGTTTGGAGCTCGGTT	720
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DB	721	AATATCTAAGAATATACATGTATGTTATGCAGCTTCCATTTTGGCAGAGCAATTAATCT	780
QY	781	AGACGAGCGAGGTTACGCTTAATGAATAGCGGCAACTTTCAAAGAGAGAGGTGATGA	840
DB	781	AGACGAGCGAGGTTACGCTTAATGAATAGCGGCAACTTTCAAAGAGAGAGGTGATGA	840
QY	841	TGTTTCTTTTCTTTTCTGCTGATGAAGTACTTTTAAATTAATAGTCATAAATACAAAATAT	900
DB	841	TGTTTCTTTTCTTTTCTGCTGATGAAGTACTTTTAAATTAATAGTCATAAATACAAAATAT	900
QY	901	CTTGCAATATGATAGTTAAATCTTACTTTCTGCTTCTAGTAGAATAGTTTACTTTAAGGA	960
DB	901	CTTGCAATATGATAGTTAAATCTTACTTTCTGCTTCTAGTAGAATAGTTTACTTTAAGGA	960
QY	961	ATTTTATGACATAGGGTTAACTTTGGTTTGTAAATTTTCAAAAGTAGATACCTATAT	1020
DB	961	ATTTTATGACATAGGGTTAACTTTGGTTTGTAAATTTTCAAAAGTAGATACCTATAT	1020
QY	1021	TCTGTACAAGAGTTTACAGAGTGGGTGTGATAGTATCAGTTCTATGAGCGGATGGA	1080
DB	1021	TCTGTACAAGAGTTTACAGAGTGGGTGTGATAGTATCAGTTCTATGAGCGGATGGA	1080
QY	1081	AGACGCTTTGCTTACAAGAAAACTTTGGCCATGTTCAACACTGAAAGAGCAATCTTTAG	1140
DB	1081	AGACGCTTTGCTTACAAGAAAACTTTGGCCATGTTCAACACTGAAAGAGCAATCTTTAG	1140
QY	1141	AGACGCGCTTCGGTTAACTTTTGGTTCCCTAGATGAAGGACATGGTATAGTACCGCT	1200
DB	1141	AGACGCGCTTCGGTTAACTTTTGGTTCCCTAGATGAAGGACATGGTATAGTACCGCT	1200

QY	1201	GTTTGAGGTTCTATTACCAGCAAAAAGATGACAAGGAGTGAAGTCAATTGTTAACTGTA	1260
DB	1201	GTTTGAGGTTCTATTACCAGCAAAAAGATGACAAGGAGTGAAGTCAATTGTTAACTGTA	1260
QY	1261	CTTCTGTTTACACAGTGCCTTAATCATATCAGAACATATCAAGCCAAAGGTTAACTTACCA	1320
DB	1261	CTTCTGTTTACACAGTGCCTTAATCATATCAGAACATATCAAGCCAAAGGTTAACTTACCA	1320
QY	1321	GAACTATATATCTTTCTGTTGAGTCTATTAAGATCCCGCTGATATAATCAATGGTGTACTGC	1380
DB	1321	GAACTATATATCTTTCTGTTGAGTCTATTAAGATCCCGCTGATATAATCAATGGTGTACTGC	1380
QY	1381	TAGTCTCAATGGGATGTAGATAAAGCAATCTCTCAACCCCTGTCAATGACTTTCTCTT	1440
DB	1381	TAGTCTCAATGGGATGTAGATAAAGCAATCTCTCAACCCCTGTCAATGACTTTCTCTT	1440
QY	1441	GCAGACTTAAGCTGGCTGGCTTCAAGACGATATAGTAATGGGAAAGTTTCGGTGTCTGA	1500
DB	1441	GCAGACTTAAGCTGGCTGGCTTCAAGACGATATAGTAATGGGAAAGTTTCGGTGTCTGA	1500
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DB	1501	TAAACCACTTCTGAACTTATTTGGGATGAGTGGGCAAAATTTTGGAAAGCTTTTCCC	1560
QY	1561	CACTATCAAGAGAGATTGGTGAGCAGGAAATCTCTGATGTAACTGTAGAAATGCTCTGAA	1620
DB	1561	CACTATCAAGAGAGATTGGTGAGCAGGAAATCTCTGATGTAACTGTAGAAATGCTCTGAA	1620
QY	1621	GATCAAGATCCAGATCTGTATGTCAATGGAAGACAGGTTTCGTAGCTGAATACACCAA	1680
DB	1621	GATCAAGATCCAGATCTGTATGTCAATGGAAGACAGGTTTCGTAGCTGAATACACCAA	1680
QY	1681	GTCGAGAGATTACCGCATCTAGATATCAAGAGAGACTTAGAAGAGCTGAGCAATGTA	1740
DB	1681	GTCGAGAGATTACCGCATCTAGATATCAAGAGAGACTTAGAAGAGCTGAGCAATGTA	1740
QY	1741	CGACCGCTTATCAGAAATATCTATCTTTAAGGCTGCTGATAATTTTCGATATCCGAAGTT	1800
DB	1741	CGACCGCTTATCAGAAATATCTATCTTTAAGGCTGCTGATAATTTTCGATATCCGAAGTT	1800
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DB	1801	CAAGACATGTCAAGGCTTTAGATGTTAGTCTGATGTGGCAGCACAGATTAATCGTTGC	1860
QY	1861	AGTGCCCGAGATAGAGGGTTTAACTCTTACTTTTCTGATAGCCAAACCGAGAGAAATGT	1920
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QY	1921	GGCTAAGGCTCTTAAAGCACGCGCTCTCAGGCGCTGCTGATGTTGTTGAAACCGACATCCGA	1980
DB	1921	GGCTAAGGCTCTTAAAGCACGCGCTCTCAGGCGCTGCTGATGTTGTTGAAACCGACATCCGA	1980
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DB	2041	AACTCATGTTTGAAGGATGCTAACTTAGAGCACAGGAGTTGGAGTCCCTCAACGATTT	2100
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DB	2101	CCATAAGGCTTCGGTGGATGTGTGATTACAAAGCAAAATGGCATCGGTTGTCTACACTGG	2160
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QY	2221	CACTGTATCAAACTATGTCAAGTCACTAAAGGATGAAGTCGGGTATGATTTCTGATTTCCAG	2280
DB	2221	CACTGTATCAAACTATGTCAAGTCACTAAAGGATGAAGTCGGGTATGATTTCTGATTTCCAG	2280
QY	2281	GGAGAAAGTTGGTGTGGGATGTCACTTTTGAAGAGTGGCTCTCTCAAAACCTGCGGCCAA	2340

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QY
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Db 2521 TGAACCCCGAAGCTTACTGCAAGATGGTACTTTGGATGGGGTGGCTGTGGTGGTGGAA 2580
QY 2581 GTACAAAGGAGATTTGAAAGATTTGATCTTTGATGAGGATTTGATCTTGGTCTCGGAAA 2640
Db 2581 GTACAAAGGAGATTTGAAAGATTTGATCTTTGATGAGGATTTGATCTTGGTCTCGGAAA 2640
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Db 2701 GGACATGTGAGAACGGTAGATTCACTTCTAATGCAATCCAAAACCCGGATCACACAGAG 2760
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QY 3181 CCAAGGAGAAACCTTTGAAGATGTGCTGGTGCAGATTGACGGCAACTCCACTGACTCT 3240
Db 3181 CCAAGGAGAAACCTTTGAAGATGTGCTGGTGCAGATTGACGGCAACTCCACTGACTCT 3240
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 Db 4621 CCATGATAAGGGAGCAATAGTGTATATGATCCCTTTGAAAGTTGATCTCCAAACTTGGGGC 4680
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RESULT 2

US-09-962-527-1
 ; Sequence 1, Application US/09962527
 ; Publication No. US20030049813A1

GENERAL INFORMATION:

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 MCCULLOCH, MICHAEL
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TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
 PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
 FROM PLANT SOURCES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howrey & Simon
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Db 3858 UGUUACUAGUAGAGAGUCUCUCAAUAGAUUGUUUAGAAAAGCAGGAAACAGUAGGC 3917
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 Qy 5521 -----CGGAAACAAAAAGAAATGGTAGTGAATATGTTAATAAT----- 5561
 Db 5535 ATCTCGAACCGGAAAAAGAGTGTATGTCGCAAGGGAATAATAGTAGTAATGATCGGTC 5594
 Qy 5562 -----AAGAAATAAATAACAGTGTGAAGAGGGTTTTTAAATTTGAGGAATTCAGGA 5614
 Db 5595 AGTCCGAACAGAACTATAGAAATGTTAAGGATTTTGGAGGAATGAGTTTAAAGAA 5654
 Qy 5615 TAATGTAAGTATGACGAGT-----CTATCGGCTCATCGAGTACGTTTTTAATCAAT 5665
 Db 5655 TAATTTAATCGATGATTCGAGGCTACTGTCCGCAATCGAATTCGTTTAA-----AAT 5711
 Qy 5666 ATGCTTTATACAACTCCGAGCCAAATTTGTTTACTATCTTCGCTTACGAGAT 5725
 Db 5712 ATGCTTTACAGTATCACTATCCATCTCAGTTCGTTCTTGTATCAGCGTGGCGGAC 5771
 Qy 5726 CCTGTGAGCTGATCAATCTGTGTACAAATGCAATGGTAAACAGTTTCAACCGCAACAA 5785
 Db 5772 CCAATAGATTAAATAATTTATGATCTAATGCTTAGGAAATCAATTTCAACACACAA 5831
 Qy 5786 GCTAGGACAAAGTCCACAGCAATTTGCGGATGCTTGAACCTGCTAGTATGACA 5845
 Db 5832 GCTCGAATGCTGTTTCAAGACAAATTCAGTGAAGTGTGGAACCTTCAACCAAGTAACT 5891
 Qy 5846 GTGAGATTTCTGATCGGATTTCTATGTATGATATTAATTCGAGCGCTTGTATCGGTTG 5905
 Db 5892 GTTAGGTTCCCTGACAGTACTTTAAGGTGTACAGGTACAAATGCGGTATTAGACCCGCTA 5951
 Qy 5906 ATCAGGGGTTTAAATAAGCTTTTATAGTAAATAAGTAATAAGAGTTGATGATCAATCAA 5965
 Db 5952 GTACAGCACTGTTAGGTGATTCGACACTAGAAATAGAAATAGAGTTGAAATCAG 6011
 Qy 5966 CCCGACCGAATACTACTGAATCGTTAAACGCACTCAGAGGGTGAAGTGTACTGTGA 6025
 Db 6012 GCGAAACCCAGCACTGCGGAAACGTTAGATGCTACTCTGAGTGAAGTGAAGCAACGGTG 6071
 Qy 6026 GCTATAGGGCTTCAATCAATAATTTGGCTAATGACTGTTGCTGGAACCTGGCATGTC 6085
 Db 6072 GCCATAGGAGCGGATTAATAATTTAATAGTAGAATTTGATCAGAGGAACCGGATCTTAT 6131

Qy 6086 AATCAAGCAGGCTTTGAGACTGCTAGTGGACTTGTCTGGACCAACAACCTCCGGTACTTAG 6145
 Db 6132 AATCGGAGCTTTTCGAGAGCTCTTCTGGTTTGGTTTGGACCTCTGGTCTCTGCAACT--- 6188
 Qy 6146 CTATTGTTGTCAGATTTCTTAAATAAAGTCGCTGAAGACTTTAAATTCAGGGTGGCTGA 6205
 Db 6189 -TGAGGTAGTCAAGATGCAATAAATAACGGAATTGTGTCGTAATCACA-CGTGGTGGC 6246
 Qy 6206 TACCAAAATCAGCAGTGGTGTCTGTCACATTAATAAATGATGTCATATCTGGATCC 6265
 Db 6247 TACGATAACGATAGTGTCTTCCCTCCACTTAATCGAAGGTTGT-GTCTTGGATCGC 6305
 Qy 6266 AACAGTTAAACCATGTGATGTATATCTGTGTATGCGTAAACATCGGAGAGGTTTCG 6325
 Db 6306 CGGGTCAATGTATATGTTTCATATACATCCGAGGCACGTAATAAAGCGAGGGTTTCG 6365
 Qy 6326 AATCTCCCTAAACCGCGGTAGCGGCCCA 6355
 Db 6366 AATCCCGCGTTACCCCGGTAGGGGCCCA 6395

RESULT 5

US-09-962-527-2
 ; Sequence 2, Application US/09962527
 ; Publication No. US20030049813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GARGER, STEPHEN
 ; HOLTZ, R. BARRY
 ; MCULLOCH, MICHAEL
 ; TURPEN, THOMAS
 ; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
 ; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
 ; FROM PLANT SOURCES

NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howrey & Simon
 STREET: 1299 Pennsylvania Avenue N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/962,527
 FILING DATE: 24-Sep-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/037,751
 FILING DATE: 10-march-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P
 REGISTRATION NUMBER: 25,277
 REFERENCE/DOCKET NUMBER: 00801.0140.999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-463-8109
 TELEFAX: 650-463-8400
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6439 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Genomic RNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-962-527-2

Query Match

38.6%; Score 2455.4; DB 10; Length 6439;

Db 4338 AGAAGACCCCTCAGGAGUUAUACCGCAGGUAUAAAAUUCUGCAUCUGGUAUCAAAGA 4397
 QY 4382 AAAAGGGGTGATGTGACTCTTTCATCGGCAATCTGTTATATAGCAGCTTCTTGGGT 4441
 Db 4398 AAGAGCGGGACGUCACGCUUAUUGGAAACACUGUGAUAUUGUGCAUCUGUUGGCC 4457
 QY 4442 TCAATGTTACCGATGGAAGAGGTCTATAAAGGTGCTTTTGTGGAGACGATTCGGTTTGG 4501
 Db 4458 UCGAUGCUUCGAGGAGAAAUAAUACAAAGGAGCCUUUUGCGUGAGCAUGAUGUCUG 4517
 QY 4502 TATTTTCCAAAGGGTTGGATTTCCCTGACATTCAGTCATGCTGCTAATCTCATGTGGAAT 4561
 Db 4518 UACUUCCAAAGGUGUGAUGUUCGGAUGUGCAACACUCCCGGAUUCUUAUUGGGAU 4577
 QY 4562 TTTGAGGCCAACTGTATAGAAAGAGTACGCTTACTTTTGTGTGATACATCATAC 4621
 Db 4578 UUGAAGCAAAACUGUUUAAAAACAGUAUGGAUAUUCUUUGCGGAUAUGUAUAU 4637
 QY 4622 CATGATAAGGGAGCAATAGTATATGATCTTTGAAAGTTGATCTCCAACTTGGGCA 4681
 Db 4638 CACGACAGAGUAGCAUGUAUUAAGUACUCCCUAAAGUAGUACUGAAACUUGUGCU 4697
 QY 4682 AAACATATCAAGATTTATGATCTATAGAAAGATTAAAGGTGCTTTTGTGCGATGTTGCT 4741
 Db 4698 AAACACAUAAGAUUGGGAACACUUGGAGGAGTUCAGAAAGGUCUCUUGUGAUGUUGCU 4757
 QY 4742 TGTTCGCTCGGAACCTGCTCTAGGCTTTCGCCAGCTGAACGACGCTATCAAGGAGTT 4801
 Db 4758 GUUUGGUAGAACAAUUGUGGUA---UUAACACAGAGUUGGACGCGUGAUGGGAGGU 4814
 QY 4802 CATAAAACCGGATTTGATGCTGCTTGTCTTTTAAATGCTTAAACAAATTTTGTGTGAT 4861
 Db 4815 CAUAGACCGCCUCCAGGUCUUGUUUAUAAAGUUGUGGUAUUAUUGUGCU 4874
 QY 4862 AAATTTTATTTAGAACTTTGTTTAAATGGCTGTTAGTCTCAGAGATACTGTCAAAT 4921
 Db 4875 AAGAGUUCUUUUAAGAGUUUUUAUAGUGGUCUAGUUGUUUAAAGAAAGUAGAAU 4934
 QY 4922 TAGCGAGTTCATTTGATCTTTCGAAACAGGATGATATCTTCGGCATTCATGACTAAGT 4981
 Db 4935 CAUAGAUUAUCGACCGUGUAAAAUUGGAGAAUUAUUAUUGGAGUUGUUAUCCCGUG 4994
 QY 4982 CAAGAGTGTAGAAATATCGACTGTGGAACAAGATTATGGCTGTGTTAAAGATGATGTTTC 5041
 Db 4995 AAGAGUUAUUGUUUCCAAAGUAGUAUAAUUAUUGGUCAUGAGAAUGAUAUGU 5054
 QY 5042 TGATGTAGATTTACTTAAAGGTGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 5101
 Db 5055 AGAGGUGAACCUUUAAGAGGUAUAGCUUAUUAUAGUGGAUACGUCUGUUUAGCCGG 5114
 QY 5102 TTTGGTAGTCTCGGGAGTGAATCTCCGGATTAATCGCTGCTGGTGGTCTAGTGTG 5161
 Db 5115 UUGUGUGUGUACCGGGCGAGUGGAACUUGCCUGAUAUUGAGAGGAGGUGUGAGUGUG 5174
 QY 5162 TATTTAGATAAGAGAAATGAAAGGAGTAAGGAGCAACGCTGGCTGCTATCACGCCCC 5221
 Db 5175 UUGUGUGAACAAGAGUAGAGAGCGGACGAGGACACUUCUGGAUUAUUAUACAGC 5234
 QY 5222 TGCTTGCAAAAGAAATTTTCTTTTAAAGCTTAATCCCTTAATTTTCAATAACATCCGAGGA 5281
 Db 5235 AGCUGCAAGAAAGAAUUAUAGUUAAGGUGUCCCAUUAUUGUAUUAUUAUUAUUAUUA 5294
 QY 5282 TGCTGAGACGACCCGTCGAGTGTAGTGAATATCAAGAGGAGTGTGCTATGAAGAGG 5341
 Db 5295 CGCGAUGAAAAACGUCUGGCAAGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5354
 QY 5342 ATACTGCTTTTCTTTGAGTTCGTTTCAATTTGTTAGTATACATAAAATTAATGTAAG 5401
 Db 5355 UUCUGUCCCUUUCUGAGUUGUGUGCGUGUGUUAUUAUUAUUAUUAUUAUUAUUAUUA 5414
 QY 5402 AAAAGGTTTGGGGAACGTTATTTTGTGAGTGTGACAGACGCTTCGCCAATTCATCTGA 5461

Db 5415 AUUAGGUUUGAGAGAGAGAAUUAACAAACGUGAGAGACGAGGGCCCAUGGAAUUAUACAGA 5474
 QY 5462 AAAAGTGTGTTGAGGAGTTCGTGATGAAGTACCAATGGCTGTGAAATCTCGAAAGGTTTC 5521
 Db 5475 AAGAGUGGUUGAGAGUUAUGGAAAGUAGUCCCUUUAUGUAGUAGCGGUUUGCAAGUUUCG 5534
 QY 5522 GG-----AAAAAAGAGAAATGGTGTAGGTAATAATGTTTAAATAAT----- 5561
 Db 5535 AUCUCGAAACCGGAAAAAGAGUGUCCCAAGGAAAAAUAUAGUAGUAAUAGUAGUAGU 5594
 QY 5562 -----AAGAAATAATAACAGTGTGTAAGAGGGTTTTTAAATTTAGAGAAATTTAGGA 5614
 Db 5595 AGUCCGCAACAAGAACUAUAGAAUUAUUAAGGAUUUUGGAGGAUUGAGUUUAAAAAGAA 5654
 QY 5615 TAAATGTAAGTGTAGCAGAGT-----CTATCGCGTTCATCGAGTACGTTTAAATCAAT 5665
 Db 5655 UAAUUUAUGAUGAUGAUUUGGAGGCUACUGUCCGCAAGUUGUUAUUGUUAUUGUUAU 5711
 QY 5666 ATGCTTTATACAACTCTCCGAGCCAAATTTGTTTACTTATCTTTCGCTTACGCAGAT 5725
 Db 5712 AUGUCUUAAGUAUACUACUCCCAUCAGUUGUGUUCUUGUACUAGCGGUGGCGGAC 5771
 QY 5726 CCGTGTGAGTGTGATCTGTGTACAAATGATTCGTTGTAACCACTTTCAACGCAACAA 5785
 Db 5772 CCAUAGAGUUAUUAUUAUUGUACUAAUGCCUUAAGGAUUAUUAUUAUUAUUAUUA 5831
 QY 5786 GCTAGGACAACTCTCAACAGCAATTTGCGGATGCTGGAAACCTGTGCTAGTATGACA 5845
 Db 5832 GCUCGAAUCUGUUCUUAAGAAUUAUAGUAGUGUGGUGGAAACUUAUUAUUAUUAU 5891
 QY 5846 GTGAGATTTCTGTCATCGGATTTCTATGTGTATAGATATAATTCGAGCGTTGATCGGTG 5905
 Db 5892 GUUAGGUUCCUGACAGUACUUAAGGUUAUAGUACAGUACUUAUUAUUAUUAUUAU 5951
 QY 5906 ATCAGCGGCTTATTAATAGCTTTGTATCTAGAAATAGATAATATAGAGTTGATATCAA 5965
 Db 5952 GUCACAGCAGUUAUAGGUGCAUUCGACACUAGAAUUAUUAUUAUUAUUAUUAUUA 6011
 QY 5966 CCGCAGCAGAACTACTGAAATCGTTAAAGCGGCTCAGAGGCTAGACGATGCTACTGTA 6025
 Db 6012 CGCAACCCACGACUCCGGAACGUAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 6071
 QY 6026 GCTATAAGGCTTCAATCAATTAATTTGGCTTAATGAATGCTGCTGGAACCTGCTGTTTC 6085
 Db 6072 GCCAUAAGGAGCGCAUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6131
 QY 6086 AATCAAGAGGCTTTGAGACTGCTAGTGTGACTGTCTGACCACTCGGCTACTTAG 6145
 Db 6132 AAUCGAGGUCUUAUUCGAGAGCUCUUGUGUUGUUGGACCUUGUGGUCGCAACCUAG 6191
 QY 6146 CTATT 6150
 Db 6192 CAUU 6196

RESULT 6

US-10-828-029-2

; Sequence 2, Application US/10828029

; Publication No. US20040171813A1

; GENERAL INFORMATION:

; APPLICANT: GARGER, STEPHEN

; HOLTZ, R. BARRY

; MCCULLOCH, MICHAEL

; TURPEN, THOMAS

; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
 ; PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
 ; FROM PLANT SOURCES

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howrey & Simon

; STREET: 1299 Pennsylvania Avenue N.W.

; CITY: Washington

; STATE: DC

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/962,527

FILING DATE: 24-Sep-2001

APPLICATION NUMBER: 09/037,751

FILING DATE: 10-march-1998

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P

REGISTRATION NUMBER: 25,277

REFERENCE/DOCKET NUMBER: 00801.0140.999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-463-8109

TELEFAX: 650-463-8400

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 6446 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: Genomic RNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-828-029-5

Query Match 38.5%; Score 2449.8; DB 17; Length 6446;
Best Local Similarity 44.8%; Pred. No. 0;
Matches 2771; Conservative 1146; Mismatches 2212; Indels 60; Gaps 8;

Qy	20	ACAACAATTAATAAACAACAATATTACAAACAACAACAACAACAACAATGGGCAC	79
Db	18	ACCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA	77
Qy	80	ATACAATCTATAATTAGCAAGCCCTTCTTGAAAGCGTGATGTAATAACATCTCTGTT	139
Db	78	ACACAGACGCUACCAACAUCAGCUUUGCUGGACACUGCCGAGGAAACAACUCCUGGUC	137
Qy	140	AATGACCTTGAAGAAGCGCATGTAGCATACGCGCTGGAAGAAATTTAACGCCCGGCAC	199
Db	138	AUGAUCUAGCAAGCGUGUCUUUACGACACACGCGGUGAAGAGUUUAACGUCUGAC	197
Qy	200	CGTAGACAAGGTCATCTTTCAAACCTATTAGCGAAGAGAAACGCTTTAGTCTCC	259
Db	198	CGCAGGCCAAGGUGAAUUUUAACAAAGAUAAAGCGAGGAGCAGCGUUUUGCUAC	257
Qy	260	AACCGCTACCGGAGTTCAGATTACCTTTTATATCTCAAAATCGGTACACAGTTG	319
Db	258	CGGCGUUCAGAAUUCCAAUUUACAAUUAUUAACACGCAAAUUGCCUGCAUCCGU	317
Qy	320	GCTGGAGTTTGAGAGCATTAGAATTGGAATATCTGATGCTACAAATTCCTATGGATCG	379
Db	318	GCAGGUGAUGCGAUCUUUAGACUGGAUAUCUGAUGCAAAUUCUCCUACGUA	377
Qy	380	CCGACATATATATAGTGGAACTTTGACGCAATTGTTTCAAAGGAGGATTACGTG	439
Db	378	UUGACUUAUGACAUGCGGAAUUUUGCAUCGCAUCUUGUUAAGGACGAGCAUAUGUA	437
Qy	440	CATTGCTGTAGCCCACTCTGGACATACGAGATATATAGGCAAGGACGAGCAAAAGGC	499
Db	438	CACUGCUGCCCAACCCUGGACUUGGAGACAUCAUGCGGACGAGGCGCAGAAAGC	497
Qy	500	TCAATTGAGATGTTTGTCCAGATTGTCTCGTTCTAACAGGTAAATTCCTGAGTTTCAA	559
Db	498	AGUAUAGACUAUACCUUUAUGCUAGAGAGAGGGGGAACACAGUCCCAACUCCAA	557
Qy	560	AGGAGGCTTTTAAACAGTATGCAAGAGCTCCCAACGAAGTCTGCTGCTCTTAAACTTTT	619
Db	558	AAGGAAGCAUUUGACAGAUACGCAAAUUCUGAAGACGCGUCUGUTCACAUAUUCU	617
Qy	620	CAGGATCTCGAATATCCGCCAGAGATAGTGGTAGAGATACGCTGTGCTCTGCAC	679
Db	618	CAGACAAUGGCAUACGACCGCAGCAUACGAGGAGAGUUGCAUUGCCUACAC	677
Qy	680	AGTTTGTATGATATTCTCTGTGATGAGTTTGGAGCTGCTGTTAAATCTAAGAATATACAT	739

Db	678	AGCAUAUAUGACAUAACAGCCGAUGAGUUCGGGCGGCACUCUUGAGGAAAAUUGUCAU	737
Qy	740	GTATGTTATGACAGCTTCCATTTTGGCAGAGCATTATTACTAGACAGAGGAGTTACG	799
Db	738	ACGUCUAGCCGCUUCCACUCUCUGAGAACCCUGCUUCUUGAAGAUCAUACGCUCAU	797
Qy	800	CTTAATGAATAGCGCCAACTTTCAAAAGAGAGAGGTGATGATGTTCTTTTCTTTGCT	859
Db	798	UUGGACGAUAUACAACCGGUGUUUUCGCGGAGGAGACAAGUUGACCUUUUUCUUUGCA	857
Qy	860	GATGAAGTACTTTAAATATTAGTCATAAATACAAAAAATATTCTTGCATTATGTTAAA	919
Db	858	UCAGAGAGUACUCUAAUUAUUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU	917
Qy	920	TCCTACTTTCTCTCTCTAGTAGAATAGTTTCTTTAAAGAAATTTTAGTCACTAGGTT	979
Db	918	ACUUAUCUCCCGCCCUUAUAUAGAGAGGUUUAUUAUAGAGAGGUUUUUAUUAUUAUUA	977
Qy	980	AATACTTGGTTTGTAAATTTTACAAAGTAGATACCTATATTCTGTACAAAGAGTGTAGA	1039
Db	978	AUAUCCUGUUUUGAAGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1037
Qy	1040	CAAGTAGGTTGATAGTATGATCTTATGAGGCGATGGAAGACGCTTTTGTCTTACAAG	1099
Db	1038	CAUAAAGUUGUAGUAGAGGAGCAGUUUAUUAUCGAAUUGGAGCAGCGCAUUAACAA	1097
Qy	1100	AAAACCTTGGCCATGTTCAACACTGAAAGAGCAATCTTTTAGACACACGCTTTCGTTAA	1159
Db	1098	AAGACUCUUGCAUUGGCAACAGCAGAGAAUCCUCCUUGAGGAUUUAUUAUUAUUAUUA	1157
Qy	1160	TTTTGGTTCCCTAAGATGAAGGACATGGTATAGTACCGCTGTTTGGAGGTTCTATTACC	1219
Db	1158	UACUGUUUCCAAAAGAGGGAUUGGUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1217
Qy	1220	AGCAAAAGATGCAAGGAGTGAGGTCAATTTGTTTAATCGTGACTTTCGTTTACACAGTC	1279
Db	1218	ACUUAUAGAGGAGCGCAAGGAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1277
Qy	1280	AATCATATCAGACATATCAAGCCAAAGGCTTAACTTACCAGAACGTTATTATCTTTCTG	1339
Db	1278	AACCAAUUCGAAACAUACAGGCGGAAAGCUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1337
Qy	1340	GAGTCTATAGATCCCGCGTGATAATCAATGGTGTACTCTAGGTCTGAATGGGATGTA	1399
Db	1338	GAAUUGAUCGAGGAGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1397
Qy	1400	GATAAAGCAATCTTCAACCCCTTGTCAATGACTTTCTTCTTGACAGCTAAGCTGGCTGCG	1459
Db	1398	GACAAAUUUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1457
Qy	1460	CTTCAAGACGATATAGTAAGGAAAGTTTCGGTGTCTTGGATTAAGACCATCTCTGAATCT	1519
Db	1458	CUAAAGGAUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1517
Qy	1520	ATTGGGATCAGGTGGGCAAAATTTTGGAAAAGCTTTTCCCACTATCAAAAGAGAGATTG	1579
Db	1518	GUGUGGAUAGAUUUCGUGGCUUUGGGAACGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1577
Qy	1580	GTGAGCAGGAAAAATTCGTGATGTAAGTGAAGATGCTCTTGAAGATCAAGATCCCAAGATCTG	1639
Db	1578	UUGAAGCAGGAAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1637
Qy	1640	TATGTCATATGGAAGACAGGTTCTGATCTGAATACACCAAGTCTGAGGAGTTACCCGAT	1699
Db	1638	UAUGUGACCUUCCACAGAUUAUGACGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1697
Qy	1700	CTAGATATCAAGAGGAGCTTTAGAAAGAGCTGAGCAAAATGTACGCGGTTTATCAGAATTA	1759
Db	1698	CUUGACUUAUAGGAAGAAUGGAAGAAACCGAAGUGAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA	1757
Qy	1760	TCTATCTTAAAGGTTGCTGATAATTTTCGATATCGGAAAGTTTCAAGACATGTGCAAGCT	1819

Db 1758 UCGUGUUAAGGAGGUCUGACAAUUCGAUUGUUGUUUUUCCAGAUUGCCAAUCU 1817
 Qy 1820 TTAGATGTTAGTCTCTGATGTGGCAGCAGAGTAATCGTTGCGAGTGGCCGAGATAGAAGC 1879
 Db 1818 UUGGAAUGUUGACCCAAUGACCGCAGCAAGGUUAUAGUCGCGGCUAUGACCAUGAGAGC 1877
 Qy 1880 GGTTTAACTCTTACTTTTGTATAGCCCAACCGAGGAAATGTGGCTAAGGCTCT- ----T 1933
 Db 1878 GGUCUGACUCUCAUUGAAGAACACCUACUGAGCGAAGUUGCGUAGCUUUAACAGGAU 1937
 Qy 1934 AAAAGCAGCGCTCTGAGGCGGTGTATGTTCTTTGAACCGACATCCGAAGAGGTGAACGTA 1993
 Db 1938 CAAGAGAAGCUUCAGAGGUGUUGUUGUUAUACCUAAGAGAAUGAAGAACCGUCC 1997
 Qy 1994 AATAAATTTCTATTGCTGAGAAAGGAGATTGCCCTGTGTGTCAGAAAGTCAATGTTTG 2053
 Db 1998 AUGAAGGUUGCGAUGGCCAGAGGAGAGUUAACAUAUAGUGGUCUUGCUGGAGAUCAUCG 2057
 Qy 2054 ACGAATGCTAACTTAGAGCACCGAGGATTGGAGTTCCTCAACGATTTCCATAGGCTTGC 2113
 Db 2058 GAGUCGUUUAUUAAGAAACGAGAGAGUAGAGUUAUAGAGCAGUUAUUAUGGCAAGC 2117
 Qy 2114 GTGGATAGTGTGATTACAAAGCAATGGCATCGGTTGTCTACATCGCTCACTCAAGTT 2173
 Db 2118 GCAGAUUGUUAUUCGUAAAGCAGAGAGCUCGUAUUGUUAACACGGGUCGUAUAAAGU 2177
 Qy 2174 CAACAAATGAAGAACTATGTGGACAGTTTGGCAGCTTCTGTTGTCGCGCACTGTATCAAT 2233
 Db 2178 CAGCAAAUGAAAAACUUUAUCGUAUGCCUGGAGCAUCAUAUCUGCGGUGUGCAU 2237
 Qy 2234 CTATGCAAGTCACTTAAAGGATGAAGTCGGGTATGATTCTGATTCCAGGGAGAAAGTTGGT 2293
 Db 2238 CUGUCAAGAUCCUCAAAGUAACAGCUGCUUAUGACCUUAGAAACCCGUCAAAGUUGA 2297
 Qy 2294 GTTTGGGATGCTACTTTGAAAAAGTGCTCTCTCAACCTGCGGCCAACAGTCAATCATGG 2353
 Db 2298 GUCUGAUGUGCAUCUAGGAAUGGUUAUUAACAACCAACGGCCAGAGCUAUGCAUGG 2357
 Qy 2354 GGATGTCCTGATTAACAAGGGAAATGTTTACTGCACTTCTATCTTATGAAGGAT 2413
 Db 2358 GGUGUUGUUAACCCACGCGAGAGUAUCAUGUGCGCGUUUUGAAUUAUGAAGAGCAG 2417
 Qy 2414 AGAATGCTGACTGAGACGCACTGAGAGGCTGGCTGTATCATCTGATACAAATGCTATAT 2473
 Db 2418 GGUGUGGACUAGCAGUAGUAGAGAGAGUAGUGCUGACUGCUGAGUCUGUUGUUAU 2477
 Qy 2474 TCTGATATGCAAGCTCCTCAAAATCTGAGGAAACCAATGAGAGACGGTGAACCCCGAA 2533
 Db 2478 UCCGACAUUGCGGAAACUCAGAAACUCUGCGCAGACUGCUUGGAAACCGGAAACCGCAUG 2537
 Qy 2534 CCTACTGCAAGATGGTACTTGTGGATGGGCTGCTGTTGTGGAAGTACAAAGGAT 2593
 Db 2538 AGUAGCCGAAGGUUGUUGUUGGAGCGAGUUCGCGGCGUGGAGAAACCAAGAAAU 2597
 Qy 2594 TTTGAAAGATTGATCTTGTAGAGATTTCATCTTGGTTCTTGGAACCAAGCTGTGCT 2653
 Db 2598 CUUUCAGGGUUAUUAUGAAGAUCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2657
 Qy 2654 ATGATCAGAGAGAGGGTAAATTCATCTGGAATGGAAGAGCCCAATGGAATGTGAGA 2713
 Db 2658 AUGAUCAGAGAGACGUGCGAAUUCUCACAGGGAUUAUUGUGCCACGAGGACCGUUA 2717
 Qy 2714 ACGGTAGATTCACTTCTTAATGCATCCAAACCCGATCAC- ----ACAAAGGCTT 2764
 Db 2718 ACCGUUGAUUUUAUGAUGAAUUUUGGAAAGACACGCGUUGUUAUUAAGAGGUUA 2777
 Qy 2765 TTTATTGATGAAGGTTGATGCTGCACACCGGTTGTGTTAACTTCTCTGCTTATCTCT 2824
 Db 2778 UUCAUUGAAGAGGUUGUUGCAUUGGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2837
 Qy 2825 GGTTCGCATCGCATCATTTACGAGATACACAGCAGATTCCTTTTCAATACAGATT 2884
 Db 2838 UUGUGCGAAAUUGCAUUAUUGUUAACGGAGACACAGCAGCAUUCUUAUUAUUAUUAUUA 2897

Qy 2885 CAGAATTTCCCGTATCCCAACATTTTGGAGCTGCAAGTGATGAAGTTGAGATGAGG 2944
 Db 2898 UCAGAUUCCCGUACCCCGCCCAUUUGCCAAUUGGAAAGUAGAGGUGGAGACACGC 2957
 Qy 2945 AGGACACACTGAGATGCGCCAGGTGATGTGAATTTTTTCTTCAATTCGAAGTACGAAGA 3004
 Db 2958 AGAAUAUCUUCUUGUUGCCAGCCAGUACACAUUAUCUUAACAGGAGAUUAGAGGCG 3017
 Qy 3005 GGGGTGACAAACACTTCAACTGTACAACGATCGGTTCTATCTGAGATGATAGCGGTAG 3064
 Db 3018 UUGUGAUGAGCACUUCUUGGUUAAAGUUGUUGCAGAGAGUUGGCGGAGGCC 3077
 Qy 3065 GGAGTACTAAACAGTGTTCCTAAACCACTTAAAGGGAATTTGTAATTTCTCACTCAGGCT 3124
 Db 3078 GCGGUAUUAUCCCAUCCUUAACCCUUGCAUGGCAAGUCCUUAUUAUUAUUAUUAUUA 3137
 Qy 3125 GATAAATTTGAGTTAGAGAGAGGCTTATAAGATGTGAACACCGTTTCATGAGATCCAA 3184
 Db 3138 GAUAAAGAGCUCUGCUUUAAGAGGGUUAUUCAGAUUGUUCACACUGUGCAUGAAGUGCAA 3197
 Qy 3185 GGAGAAACCTTTGAAGATGTGTGCTGTCAGATTGACGGCACTCCACTGATCTGTATT 3244
 Db 3198 GCGGAGACAUACUCUGAUGUUAUCUAGUAGGUUAACCCUACACCGAGUCUCAU 3257
 Qy 3245 TCCAAGTCTTCCCGCATGTTCTAGTCGCTCTGACTAGACACACAAAGAGTTCCTCAATAT 3304
 Db 3258 GAGAGACAGCCCAUUAUUGGCAUUGUUAAGGCAACGACACACUUGUUGCUCAAGUAC 3317
 Qy 3305 TACACGCTAGTGTAGTCTTTAGTACAGATAAATAGTGTGTTCTTTTAAAGTCTC 3364
 Db 3318 UACACUGUUGUUAUGAUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3377
 Qy 3365 TTCTTTTGAATGTATGTATGTAAGCAGGTAGTAGATGCAATTCAGATGATGCA 3424
 Db 3378 UACUUGUUAUGUUAUUAAGUUGCAUGCAGGAGAAACAAUUAUGAUAUUAUUAUGAUG 3437
 Qy 3425 GTGTTCAAAAGTCAATCTCTTTGTGCAACACCTTAAATCAGGAGACTTTCAGATCTA 3484
 Db 3438 GUGUUAAGGUUCCNAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3497
 Qy 3485 CAGTTCTATTAAGATGTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3544
 Db 3498 CAGUUUAUUAUGAUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUGUUG 3557
 Qy 3545 GTTACCATGAGTTAGTGTATGATCTTAAATGTGAAGGATGCTTCTGATTTTCTC 3604
 Db 3558 GUUACCAUGAGGUUGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3617
 Qy 3605 AAAAGTATTCCGATGCCAAGAGGTGAACCATGTCTAGAGCCAGTTTTCGCTACCGCG 3664
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 Qy 3665 GCGGAAACCCGCAAGGCTGAGACTCTCGAAAAATCTGGTTGCAATGATTAAGAAAT 3724
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 Qy 3845 GTGATCAGAGATTCAATGATGATGTTGGAAAAACAGGAAAGATCTATTGAGAC 3904
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 Qy 3905 GACTTCGCTAACTACAAATTTTACAGATCTGCGGGCATCTGATCAGTACAGACATGATC 3964
 Db 3918 CAGCUCGAGAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3977

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 QY 620 CAGGATTTGCGAATACATCCGCCAGAGAAATAGTGGTAGAAGATACGCTGTGCTCGCAC 679
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 QY 680 AGTTTGTATGATATCTCTGTGATAGTTTGGAGCTGCGTTATATCTAAGAAATATACAT 739
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 QY 740 GTATGTTATGACGCTTCCATTTTGGCAGAAAGCAATATTACTAGACGAGGAGTTACG 799
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 QY 860 GATGAAAGTACTTTAAATATAGTATCAATAACAAATATCTTGCATTATGTAGTTAAA 919
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 QY 1400 GATAAAGCAATCTTCAACCTTGTCAATGACTTTCTTCTGAGACTAAGTGGCTGCG 1459
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 Db 1938 CAAGAGAGGCUUCAGAGGUGCUUUGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUA 1997
 QY 1994 AATAAATTTCTTATGCTGAGAAAGGAGATTGCTGTGTGTCGCAAAAGTCAATGCTT 2053
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 QY 2054 ACGAATGCTTAACTTAGAGCACCAGAGGTTGGAGTCCCTCAACGATTTCCATAGGCTTGC 2113
 Db 2058 GAGUCGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2117
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 Qy 440 CATTGCTGTATGCCCAATCTGGACATACGAGATATATGAGGACGAGGACGAGCAAAAGGAC 499
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Db 4098 ACTAGGCAATTTACTGCGACAGTGTGATTCGACAGATTTTGTGTTTTCACAAAGAAACA 4157
QY 4142 CCAGAACAGATTCAGAAATTTTCTCGGATCTCGACTCGCACTGCTATGATGATGTTA 4201
Db 4158 CAGCGCAGATTTGAGATTTCTTCGAGATCTCGACAGTCAATGTCGCGATGATGCTTTG 4217
QY 4202 GAACCTGATTTTCTAAGTATGATTAAGTCAAGAACGAGTTTCTATGCTGCTAGATAT 4261
Db 4218 GAGCTGATATCAAAATACGACAAATCTCAGAAATGAATTCACCTGCTGCTAGATAT 4277
QY 4262 GAAATATGAAAGATTTGGTCTCAATGATTTTGGCGGAGTGTGAAACCAAGGCAAC 4321
Db 4278 GAGATCTGGCGAAGATTTGGGTTTGAAGACTTCTTGGGAGAAAGTTTGGAAACAAGG 4337
QY 4322 AGGAAACCAACTTTGAAGGATTTACATTTGCTGGAATCAAGACATGCTGTGTTATCAAAG 4381
Db 4338 AGAAGACCACTCTCAGGATTTACCGCAGGATTAAGAACTTGCATCTGGTATCAAAGA 4397
QY 4382 AAAAGCGGTGATGATGATCTTTCTATCGGCAATATCTGTTATTAATAGCAGCTTCTGGGT 4441
Db 4398 AAGAGCGGGAAGTCAAGCAGTTTCAATTTGAAACACCTGATCATTTGCTGCTATTTGGCC 4457
QY 4442 TCAATGTTACCGATGGAAGGTCATAAAGGTTGCTTTTGGAGACGATTTCCGTTTGG 4501
Db 4458 TCGATCTTCGATGGAAGAAATTAATCAAGAGGCTTTTGGTGACGATGCTGCTG 4517
QY 4502 TATTTTCAAAGGTTTGGATTTCCCTGATTCATTCAGTCAATTCAGTCAATCTCTGTTGGAAT 4561
Db 4518 TACTTTCAAAGGTTTGTGATTTCCGATGTGCAACACTCCGCGAATCTTATGTGGAAT 4577
QY 4562 TTTGAGGCCAACTGATGAGAGAGGTACGGTTACTTTTGTGGTAGATACATCATACAC 4621
Db 4578 TTTGAGACAAACTGTTTAAAGAAACAGTATGGATCTTTTGGGAAAGATATGTAATACAT 4637
QY 4622 CATGATAAGGCAATAGTATGATTTGATCTCTTTGAAAGTTGATCTTCAAACCTTGGGCA 4681
Db 4638 CACGACAGAGGATGCTTTGTTATTCAGTCCCTTAAAGTTGATCTCGAACTTGGTCT 4697

[illegible]

Db	4218	GAGCTGATATATCAAAATA	CGACAAATCTCAGATGA	AAATCCACTGTGCAGTAGAATAC	4277	
Qy	4262	GAATAATGGAAAAAGATTGGGTCT	CAATGAGTTTTTGGCCGGAAGTGTG	GAAAAAAGGGCCAC	4321	
Db	4278	GAGATCTGGCGAAGATTGGGTTT	GAAGACTTCTTGGGAGAGTTTGG	AAACDAAGGGCAT	4337	
Qy	4322	AGGAAACAACTTTGAAGGATTA	CATTGCTGGGAATCAAGACATG	CTGTGTGGTATCAAAAGG	4381	
Db	4338	AGAAAGACCACCCCTCAAGGATTA	TACCGCAGGTATAAAACTTG	GCATCTGGTATCAAGA	4397	
Qy	4382	AAAGCGGTGATCTGACTCTTT	CATCGCAACTATGTTATAT	ATAGACGCTGCTTTGGGT	4441	
Db	4398	AAGAGGGGACGTCACAGCTTCAT	TGGAAACACTGTGATCA	TCTCGCATGTTTGGCC	4457	
Qy	4442	TCAATGTTCCCGATGGAAAGGT	CATAAAAGGTCTTTTGTG	GAGACGATCCGTTTTTG	4501	
Db	4458	TCGATGCTTCGGATGGA	AAAAATAACNAAGGACCTTT	TGCGTGACGATAGTCTGCTG	4517	
Qy	4502	TATTTTCAAAGGGTTTGGATTCC	TGACATTCAGTCA	TGTGTCATCTCATGTGGAAT	4566	
Db	4518	TACTTTCAAAGGGTTGTGAGTT	TCCGGATGTGCAACACTCC	CGGAATCTTATGTGCGAAT	4577	
Qy	4562	TTTGAAGCCAACTGTATAG	AAAGAGTACGGTTACTTTG	TGGTAGATACATCATACAC	4621	
Db	4578	TTTGAACAAACTGTTTTAAAA	CAAGTAGTAGATCTTTT	TGCGGAAGATGTGTAATACAT	4637	
Qy	4622	CATGATAAGGGAGCAATAG	TGTAATATGATCCCTTT	TGCAAGTTGATCTTCCAACTTGGGGCA	4681	
Db	4638	CACGACAGAGATGCATTTG	TATTAACGATCCCTTAA	GTTGATCTCGAACTTGGTGCT	4697	
Qy	4682	AAACATATCAAGGATTATGAT	CACTTAGAAGATTAAAGGTG	CTTTTGTGCGATGTTGCT	4741	
Db	4698	AAACACATCAAGATTGGGA	CAACTTGGAGAGTTCAGA	AGGGTCTCTTTGTGATGTTGCT	4757	
Qy	4742	TGTTGCTCGGAACTGGTGCT	TAGGCTTTCCGACGCTGAA	CCGACGTATCAAGGAGTT	4801	
Db	4758	GTTTCGTT---GAACAA	TGTGCGTATTACACACAG	TGTGGACGACCTGTATGGGAGTT	4814	
Qy	4802	CATAAAACCGGATTGATG	GTTCGTTGCTTTTAA	TGTGTTAAACAAATTTTTTGTCTGAT	4861	
Db	4815	CATAAGACCCCTCCAG	GTTCGTTTGTATTA	AAAGTCTGGTGAAGTATTTTGTCTGAT	4874	
Qy	4862	AAATTTTATTTAGAACTTT	GTGTTTTTAAATGGCTGTT	TAGTCTCAGAGATAC	TGTCAAAAT	4921
Db	4875	AAAGTCTTTTGAAGTTTG	TTTATATAGATGGCTCT	TAGTTGTTTAAAGGAAAAAGTGAATAT	4934	
Qy	4922	TAGCGAGTTCATTGATCT	TTTCGAAAAACAGATGAGAT	ACTTCCGGCAATTCATGCTAAGGT	4981	
Db	4935	CAATGAGTTTATCGAC	CTGCAAAAAATGGAGAAGAT	CTTACCGTCGATGTTTACCCCTGT	4994	
Qy	4982	CAAGAGTTTAGAATATCG	ACTGTGCAAGAATATATGG	CTGTTTAAAGAATGATAGTCTTTC	5041	
Db	4995	AAAGAGTTTATGTGTT	CCAAAGTTGATTAATAAT	TGGTTTCATGAGATGAGTCATGTTC	5054	
Qy	5042	TGATGTAGATTTTACTTA	AAAGGGTGTAAAGT	TAGTTTAAAGAGGGTATGTGTCTTAGCTGA	5101	
Db	5055	AGAGTGAACTTCTTTAA	AGGAGTTAAGCTTAT	TGATAGTGGATACGTCTGTGTTTACCCCG	5114	
Qy	5102	TTTGGTAGTGTCTGGGGAG	TGGGAATCTCCCGGATA	ACTGCCGTGGTGGTGTCAGTGTTTG	5161	
Db	5115	TTTGGTTCGTACCGGGCG	AGTGGAACTTGGCTG	CAATTCGACAGGAGGTGTGAGCGGTG	5174	
Qy	5162	TATTGTAGATAAGAGAT	AAAAAGGAGTAGAGGA	AGCAACGCTGGGTGCGGTATCACGCCCC	5221	
Db	5175	TCTGGTGGACAAAAG	ATGGAAGACCGACGAGGCCA	CTCTCGGATCTTATCAACAGC	5234	
Qy	5222	TGCTTCGAAAAAGAA	TTTTTTCTTTTAAGCTTA	ATCCCTTAATTTCAATAACATCCGAGGA	5281	
Db	5235	AGCTGCAAGAAAGAT	TTTTCAGTTC	CAAGTCTGCTCCCAATATGCTATAACCA	CCAGGA	5294
Qy	5282	TGCTGAGAGCA	CCCGTGGCAAGTGT	TAGTGAATATCA	AAAGGAGTGGCTATGGAAGAGG	5341
Db	5295	CGGCATGAAAAAGCT	CTGGCAAGTTTTT	TAGTTAATATAGAAAT	TGTGAAGATGTACAGGGG	5354

Db	1578	TTGAACAGGAACTTATCAGAGTGGCAGGCGACGCAATAGAGATCAGGGTGCCTGATCTA	1637	Db	2658	ATGATCAGAGACGTGCGAATTCCTCAGGGATTAATTTGTGGCCACGAGGACAAGCTTTAAA	2717
Qy	1640	TATGTCATGGAAGACAGCTTCGTAGCTGAATACACCAAGTCTGAGGAGTTACCCGAT	1699	Qy	2714	ACGGTAGATTCACCTTCTAATGCAT-----CRAAAACCGGATACACACAAGAGGCTT	2764
Db	1638	TATGTGACCTTCCACGACAGATTTAGTGAATGAGTACAGAGGCTCTGTGGACATGCGCTGCG	1697	Db	2718	ACGGTTGATTTCTTTTCATGATGAATTTTGGAAAGACACGCTGTCAAGTCAAGAGGTTA	2777
Qy	1700	CTAGATATCAGAAAGGACTTAGAAGAAAGCTGAGCAAAATGTACGACGGCTTATCAGAAATTA	1759	Qy	2765	TTTATTTGATGAAGGGTTGATGTCGACACACCGTGTGTAACTTTCCTGGTGCCTTATCTCT	2824
Db	1698	CTTGACATTAGGAAGAGATGGAAGAAAGCGAAGTGTATACATGCACITTCAGAGTTA	1757	Db	2778	TTCAATTTGATGAAGGGTTGATGTTGCATCTGTTGTGTAAATTTCTTGTGGCGATGCA	2837
Qy	1760	TCTATCCTTAAGGTGCTGATAATTTGATATCCGGAAGTTTCAAGACATGTGCAAGGCT	1819	Qy	2825	GGTTGGACATCCGATACATTTACGGAGATACACAGCAGATTCCTTTTCATTAACAGAGTT	2884
Db	1758	TCGGTGTAAAGGGAGTCTGACAAATTCGATGTTGATGTTTTCCTCCAGATGTGCCAATCT	1817	Db	2838	TTGTGCGAAATTCATATGTTTACGGAGACACACAGCAGATTCATACATCAATAGAGTT	2897
Qy	1820	TTAGATGTTAGTCTGATGTCGACGACGAGTATCGTTCAGTGGCGGAGATAGAGC	1879	Qy	2885	CAGAAATTTCCCGTATCCCAACATTTTGAAAGCTGCAAGTGGATGAAGTTGAGATGAGG	2944
Db	1818	TTGGAAGTTGACCAATGACGCGACGAGGTTATAGTCGGGTCATGAGCAATGAGAGC	1877	Db	2898	TCAGGATTTCCCGTACCCCGCCCATTTTGCCTAAATTTGGAAGTTGACGAGTGGAGACACG	2957
Qy	1880	GGTTTAACTCTTACTTTTGTATGATGAAACCGAGGAGATGTGGCTAAGGCTCT-----T	1933	Qy	2945	AGGACACACCTGAGATGCCAGGTGATGTGAATTTTTTCTTACAANTCGAAGTACGAAGGA	3004
Db	1878	GGTCTGACTCTCACATTTGACGACCTACTGAGGCGAATGTTGCGCTAGCTTTACAGAT	1937	Db	2958	AGAACTACTCTCGTGTGTCAGCGGATGTACACATTTATCTGAACAGGAGATATGAGGCG	3017
Qy	1934	AAAAGCAGCGGCTCTGAGCGCGTGGTATGTTCTGAAACCGACATCCGAGAGGTGAACGTA	1993	Qy	3005	CGCGTGACACCACTTCAACTGTACAAAGTACCGTCTCATCTGAGATGATAGGGGTAAG	3064
Db	1938	CAAGAGAGGCTTCAGAGAGTGTCTTGGTGTAGTTACCTCAAGAGAGTTGAAGAACCGTCC	1997	Db	3018	TTTGTCTATGAGCACTCTCTCGGTTAAAGAGTCTGTTTCGACGAGAGATGGTCGGCGAGCC	3077
Qy	1994	AATAAATTTCTATTTGATGAGAGGAGGATGTGCTGTGTGTCGAGAAATGCTAGTTG	2053	Qy	3065	GGAGTACTAAACAGTGTTCCTCAACCACTAAAGGGGAAATTTGTAACCTTTCACCTCAGGCT	3124
Db	1998	ATGAGGGTTGATGCGGACAGGAGAGTTACAAATAGTGTGCTGTTGCTGAGATCATCCG	2057	Db	3078	CGCGTATCAATCCGATCTCAAAACCTTCGATGCGCAAGATCCTGACTTTTACCCTAATCG	3137
Qy	2054	ACGAATGCTAACTTAGAGCACGAGGTTGGAGTCCCTCAACGATTTCCATAGGCTTGC	2113	Qy	3125	GATAAATTTTGAGTTAGAGGAGAGGGCTATAAGAAATGTGAACACCGCTTCATGAGATCCAA	3184
Db	2058	GAGTCGCTTATTCAAGACGAGGAGATAGAGTCTTTAGAGCAGTTTCATATGGCAAG	2117	Db	3138	GATAAAGAGCTCTGCTTTCAAGAGGGTATTAGATGTTTCCACATGTCATGAAGTCA	3197
Qy	2114	GTGATAGTGTGATTAACAAAGCAATGGCATCGGTGTGTCTACATGCTCACTCAAAAGTT	2173	Qy	3185	GGAGAAACCTTTGAAAGATGTCGCTGTCAGATTTGACGGCAACTCCTCACTGATCTGAT	3244
Db	2118	GCAGATTCGTTAAATTCGTAAAGCAATGAGCTCGATTTGTACACGGGTCGATTAAGTT	2177	Db	3198	GGCGAGACATCTCTGATGTTTCACTAGTTAGGTTAAACCCCTACACAGTCTCCATCAT	3257
Qy	2174	CAACAAATGAGAACTATGTGGACAGTTTGGACGCTTCGTTGTCGGCACTGATCAAT	2233	Qy	3245	TCCAAGTCTTCCCGGATGTTCTAGTCGCTCTCACTAGACACACAAAGAGCTTCAAAAT	3304
Db	2178	CAGCAATGAAAACTTTATCGATAGCTGATGATGATGATGATGATGATGATGATGATG	2237	Db	3258	GCAGGAGACAGCCCATGTTTGGTCGCAATTTGTCAGGACACACTGTCGCTCAAGTAC	3317
Qy	2234	CTATGCAAGTCACTAAAGGATGAAGTGGGTATGATTCGATTCAGGAGAGAAAGTTGGT	2293	Qy	3305	TACACCGTAGTGTAGATCCTTTAGTACAGATAAATTAGTGATTTGCTCTTTTAAAGCTCC	3364
Db	2238	CTCGTCAAGATCCCTCAAGATACAGCTGCTATTGACCTTGAAACCCGCTCAAGTTTGA	2297	Db	3318	TACACTGTTGTTATGATCCTTTTAGTTAGTATCATTTAGATCTTAGAGAACTTAGCTCG	3377
Qy	2294	GTTTGGGATGTCATTTTGAAAGTGGCTCTCAAACTCGGGCCAAAGGTCATTCATGG	2353	Qy	3365	TTCTTTTGAAGATGATATGTTAGTGAAGAGGAGTGTAGATAGCAATTTACAGATGGATGCA	3424
Db	2298	GTCTTGGATGTTGCATCTAGGAAGTGGTTAATCAACCAACCGGCAAGAGTCAATGATGG	2357	Db	3378	TACTTGTAGATATGATAGGTCGATGCGAGGAACCAATAGCAATTTACAGATTTGACTCG	3437
Qy	2354	GGAGTTCCTGGATTAACGGGGAATGTTTACTGCACTTCTATCTTATGAGGAGAT	2413	Qy	3425	GTGTTCAAAAGGTCATATCTCTTTTGGCAACACCTTAAATCAGGAGACTTTCCAGATCTA	3484
Db	2358	GGTGTGTTGAAACCCACCGCAGAGAGTATCATGTGGGCTTTTGGAAATATGATGAGCAG	2417	Db	3438	GTGTTCAAAAGGTTCCCAATCTTTTGTGTCAGGCCCAAGAGCTGGTGATATTTCTGATATG	3497
Qy	2414	AGAAATGCTGATGAGAGCAGCTGAGAGAGGCTGCTGATCATCTGATACAAATGGTATAT	2473	Qy	3485	CAGTTCTATTACAGTGTATGCTCCCTCGTGTGTAATAGTACTATCTTAAACAGTATGATGCT	3544
Db	2418	GGTGTGTTGACATCGGATGATTTGGAAGAGTACTGTGCTGAGTCTGTTGTTTAT	2477	Db	3498	CAGTTTTTACTATGATAAGTGTCTCCCGAGCAACAGCACCATGATGAATTAATTTGATGCT	3557
Qy	2474	TCTGATATTTGAAAGTCCAAATTTCTGAGGAAACCAATGAGAGACGTTGAACCCCGCAA	2533	Qy	3545	GTTTACCATGAGGTTAGTGTATATAGTCTTAAATGTGAAGGATTTGTTGTTGATTTTCC	3604
Db	2478	TCCGACATGCGGAACTCAGAACTCTGCGCAGACTGCTTCGAAACCGGAGAACCGCATGTC	2537	Db	3558	GTTTACCATGAGGTTGATGATGATTTTCAATTTTCAAGATTTGCAATTTGGATATGCTCT	3617
Qy	2534	CCTACTCAAGAGTGGTACTTGTGATGGGTCGCTGTTGTGGAAGTACAAAGGAT	2593	Qy	3605	AAAAGTATTTCCGATGCCAAGAGGAGTGAACACCATGCTAGAGCCAGTTTTCGTCACCGCG	3664
Db	2538	AGTAGCGAAAGGTTGTTCTTTGAGCGAGGTTCCGGGCTGTGGGAAACCAAGAAAT	2597	Db	3618	AACTGTTGCTCGGCTTAAGGATCAAAATCAACCACTAATATCTATGTTACGAAACGCGG	3677
Qy	2594	TTTGAAGATTTGATCTTTGATGAGGATTTGATCTTTGTTCTGCGAAACCAAGCTGCTGCT	2653	Qy	3665	GCAGAAACCGCAAGGCTGAGGACTACTCGAAAACTCTGTTGCAATGATTTAAAGAAAT	3724
Db	2598	CTTTCCAGGGTTAATTTTGTAGAGATCTAATTTTGTAGTACTTGGAGAGCAGCGCGGAA	2657	Db	3678	GCAGAAATGCCAGCGCAGACTGAGCTATTTGAAAAATTTAGTGGCGATGATTTAAAGGAAC	3737
Qy	2654	ATGATCAGAAAGGGCTAATTTCAATCTGGACTGATTAAGGCCAATTTGGAATTTGATGAGA	2713	Qy	3725	TTCAACGCGACCAAGCTGAGCGGAGAGATTTGAATTTGAGAGCAGCGCATCTGTTGATGTA	3784
Db				Db	3738	TTTAAACGCGACCGAGTTGCTGCGCATCAATGATATTTGAAAAATTAATGATCTTCTAGTTGTA	3797

QY	3785	GATAAGCTTTTTCATAGCTATTTTATTTAAAAAAGAAAAATACACAAAAAATATTGCTGGA	3844
Db	3798	GATAAGCTTTTTCATAGCTATTTGCTTTAAAGAAAAAGAAACCAAATAAAAAATGTTTCT	3857
QY	3845	GTGATGACGAGGATTCAAATGATGAGATGGTTGGAAAAACAGGAAGAAGTACTATTGGAC	3904
Db	3858	TTGTTCAGTAGAGAGTCTCTCAATAGATGGTTAGAAAAAGCAGGAACAGGTAAACAATAGC	3917
QY	3905	GACTTCGGTAACCTACAAATTTTACAGATCTGCGGGCCATCGATCAGTACAGACACATGATC	3964
Db	3918	CAGCTCGCAGATTTTGATTTTGTAGATTTTGCACGAGTTGATCAGTACAGACACATGAT	3977
QY	3965	AAGGCTCAACCAAAAAAGAAAAATTTGACCTTTCAAATTCAGAAATGAATACCTGCTCTGCAA	4024
Db	3978	AAAGCACAAACCAGCAAAAAATTTGGACACTTCAATCCAAACGGAGTACCCGGCTTTGCAG	4037
QY	4025	ACAATTGTCTACCAATTCGAAGACAGATCAACGGTATTTTGGCCGGTTTCT---CAGAGCTT	4081
Db	4038	ACGATTTGTGTACCAATTCAAAAAAGATCAATGCAATATTTGGCCCGTTGTTTGTAGTGAGCT	4097
QY	4082	ACAAGTTGCTGCTCGAGGCATTTGATCTTAAGAGTTTCTTTTCTTTTACTAGAAAACT	4141
Db	4098	ACTAGGCAATTAATGACAGTGTGATTCGAGCAGATTTTGTGTTTTTTCAGAAAGACA	4157
QY	4142	CCAGAACAGATTCAGAAATTTTTCTCGATCTCGACTCGCACGTTTCTATGGATGTGTTA	4201
Db	4158	CCAGCGCAGATTCAGGATTTCTTTGGAGATCTCGACAGTCACTGCGCGATGGATGCTTG	4217
QY	4202	GAATCGGATATTTCTAAGTATGATAGTCACAGAACGAGTTTCATTTGCTGCTAGAGTAT	4261
Db	4218	GAGCTGGATATACAAATACGACAAATCTCAGAATGAATTCACCTGTGCAGTAGAATAC	4277
QY	4262	GAATAATGGAAGAGATTGGGTCTCAATGAGTTTTTGGCCGAAGTGTGGAACAAAGGCCAC	4321
Db	4278	GAGATCTGGCGAGATTGGGTTTTGAAGACTTCTTGGGAGAGTTTGGAAAAAGGGCAT	4337
QY	4322	AGGAAAACTATTGGAAGGATTAATGCTTGGAAATCAAGACATGCTGTGGTATCAAAGG	4381
Db	4338	AGAAAGACCACCTCTAAGGATTAATACCGCAGGTATAAAAACTTGCTATCAAAGA	4397
QY	4382	AAAAGCGTGATGTACTACTTTTCATCGGCAATACTGTTATATACAGCTTCTGTTGGT	4441
Db	4398	AAGAGCGGACGTCACGAGCTTCATTTGGAACACCTGTGATCAATGCTCATGTTTGGCC	4457
QY	4442	TCATGTTACCGATGGAAAAAGGTCATAAAAAGTGCTTTTTGTGGAGCAGTCCGTTTTG	4501
Db	4458	TCGATGCTTCCGATGGAGAAAAATACAAAGGAGCTTTTTCGCGTGACGATAGTCTGCTG	4517
QY	4502	TATTTTCCAAAGGGTTTGGATTTCCCTGACATTCAGTCATGTGCTTAATCTCATGTGGAAT	4561
Db	4518	TACTTTCCAAAGGGTTGTGATTTCCGGATGTGCAACACTCCCGCAATCTTATGTGGAAT	4577
QY	4562	TTTTGAGCCCAACTGTATAGAAAGAGTACGTTTACTTTTGTGTAGATACATCATACAC	4621
Db	4578	TTTGAAGCAAACTGTTTTAAAAACAGATATGATACTTTTTCGGAAGATATGTAATACAT	4637
QY	4622	CATGATAAGGGAGCAATAGTGTATTAATGATCTTTTGAAGTTGATCTCCAAACTTGGGCA	4681
Db	4638	CACGACAGAGGATGCAATGTGTATTAACGATCCCCCTAAAGTTGATCTCGAAACTTGGTGCT	4697
QY	4682	AAACATATCAAGGATTAATGATCACTTAAAGAGATTAAAGGTGCTTTTGTGCGATGTGCT	4741
Db	4698	AAACACATCAAGGATTTGGAACTCTTGAGAGAGTTTCAGAAAGGTCTCTTTGTGATGTGCT	4757
QY	4742	TGTTTCGCTCGGAACTGTGCTTAGGCTTTTCCGAGCTGAACGAGCTATCAAGAGGTT	4801
Db	4758	GTTTTCGTT---GAACAATTGTGCGTATTAACACAGTTTGAACGAGCTGTATGGAAGTT	4814
QY	4802	CATAAAACCCGATTTGATGGTTTCGTTTCTTTTAAATTTGTGTTAAACAAATTTTGTGTGAT	4861
Db	4815	CATAAGACCCGCTTCCAGGTTTCGTTGTTTATATAAAGTCTGGTGAAGTATTTCTCTGAT	4874

Search completed: January 17, 2005, 21:46:50
Job time : 2273.61 secs